



Results of BLAST

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paper  
#10

BLASTP 2.2.1 [Apr-13-2001]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1006356104-14842-14592

**Query=**

(131 letters)

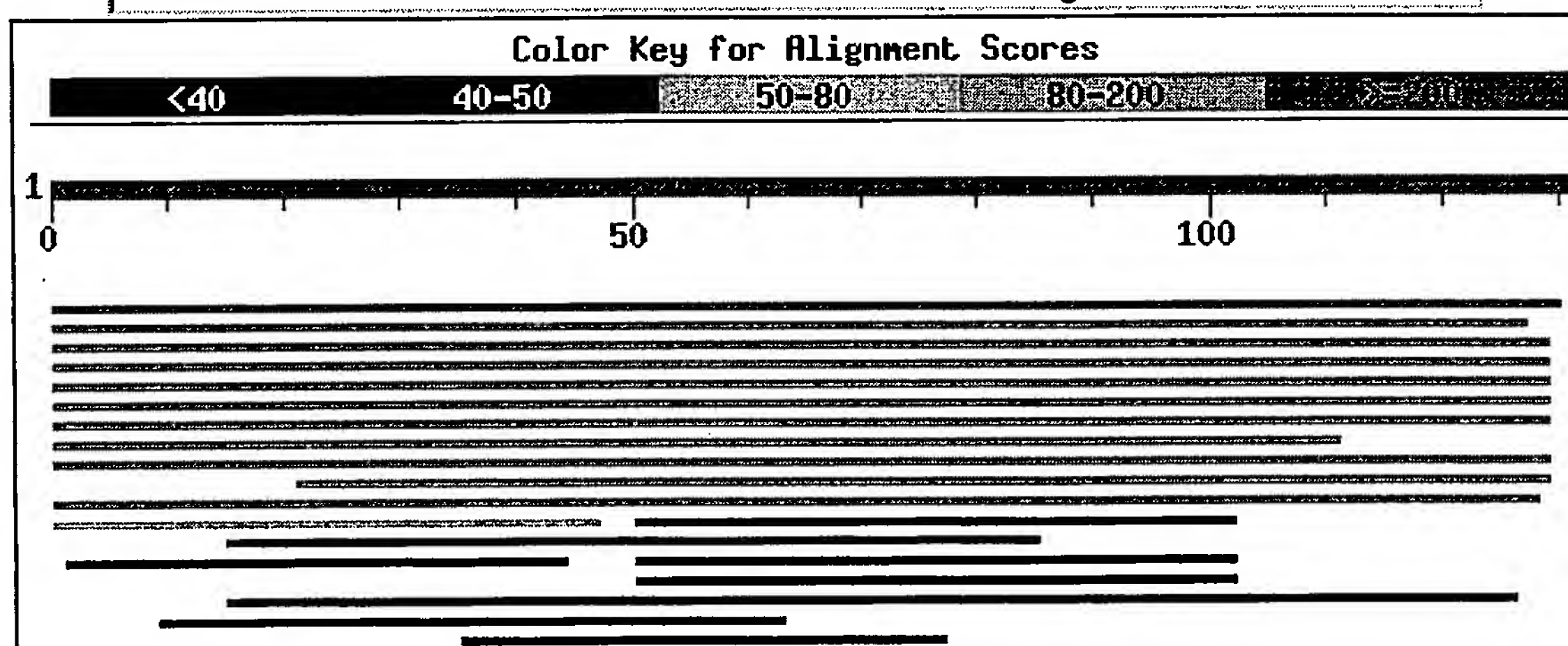
**Database: nr**

799,241 sequences; 254,026,857 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 20 Blast Hits on the Query Sequence**

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

gi 7528274 gb AAF63204.1 AF244915_1 (AF244915) interleukin-...	244	1e-64
gi 14573528 gb AAK68108.1 AF385625_1 (AF385625) interleukin...	179	4e-45
gi 2905620 gb AAC03535.1  (AF043334) interleukin 13 precurs...	169	4e-42
gi 4504645 ref NP_002179.1  (NM_002188) interleukin 13 [Hom...	169	5e-42
gi 2144691 pir A47481 interleukin-13 precursor - human >gi...	167	1e-41

gi 7387804 sp Q9XSV9 IL13_BOVIN	INTERLEUKIN-13 PRECURSOR (I...	161	8e-40
gi 1127548 gb AAA83738.1	(U10307) interleukin 13 [Homo sap...	160	1e-39
gi 4558814 gb AAD22748.1 AF072807_1	(AF072807) interleukin-...	146	3e-35
gi 6680403 ref NP_032381.1	(NM_008355) interleukin 13 [Mus...	143	3e-34
gi 14719448 pdb 1GA3 A	Chain A, Nmr Structure Of Interleuki...	141	1e-33
gi 16758680 ref NP_446280.1	(NM_053828) interleukin 13 [Ra...	139	4e-33
gi 258577 gb AAB23881.1	P600 homolog [human, Peptide, 49 aa]	61	1e-09
gi 451840 gb AAA61629.1	(U05203) putative preprosperminoge...	31	1.8
gi 16760873 ref NP_456490.1	(NC_003198) flagellar transcri...	31	1.8
gi 7387658 sp O52222 FLHC_SALTY	FLAGELLAR TRANSCRIPTIONAL A...	30	2.8
gi 16765266 ref NP_460881.1	(NC_003197) regulator of flage...	30	2.9
gi 14485571 gb AAK63010.1 AF320026_1	(AF320026) heme oxygen...	30	3.6
gi 11466430 ref NP_038436.1	(NC_002186) putative plastid d...	30	4.4
gi 1293576 gb AAA98646.1	(U49765) immunoglobulin heavy cha...	30	5.4
gi 15641617 ref NP_231249.1	(NC_002505) conserved hypothet...	29	8.0

## Alignments

>gi|7528274|gb|AAF63204.1|AF244915\_1 (AF244915) interleukin-13 [Canis familiaris]  
Length = 131

Score = 244 bits (622), Expect = 1e-64  
Identities = 131/131 (100%), Positives = 131/131 (100%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG 60  
MALWLTVVIALTCLGGLASPSVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG  
Sbjct: 1 MALWLTVVIALTCLGGLASPSVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAG 60

Query: 61 MYCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120  
MYCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY  
Sbjct: 61 MYCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120

Query: 121 VRGVYRHGNFR 131  
VRGVYRHGNFR  
Sbjct: 121 VRGVYRHGNFR 131

>gi|14573528|gb|AAK68108.1|AF385625\_1 (AF385625) interleukin-13 [Sus scrofa]  
gi|14594692|gb|AAK68109.2|AF385626\_1 (AF385626) interleukin-13 [Sus scrofa]  
Length = 131

Score = 179 bits (454), Expect = 4e-45  
Identities = 96/131 (73%), Positives = 108/131 (82%), Gaps = 3/131 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPT-LKELIEELVNITQNQAS-LCNGSMVWSVNLT 58  
MALWLT+VIALTC GGLASP PV P T LKELIEELVNITQNQ + LCNGSMVWSVNLT  
Sbjct: 1 MALWLT LVIALTCFGGLASPGPVPPHSTALKE LIEELVNITQNQKTPLCNGSMVWSVNLT 60

Query: 59 AGM-YCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNL 117  
M YCAALES LIN+SDCSAIQ+TQRM LALCS KP + Q+ + RDTKIEV Q VK+L  
Sbjct: 61 TSMQYCAALES LINISDCSAIQKTQRM LSALCSHKPPSEQVPGKHIRDTKIEVAQFVKDL 120

Query: 118 LTYVRGVYRHG 128  
L ++R ++RHG  
Sbjct: 121 LKHLRMIFRHG 131

>gi|2905620|gb|AAC03535.1| (AF043334) interleukin 13 precursor [Homo sapiens]

Length = 132

Score = 169 bits (428), Expect = 4e-42

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

```

Query: 1  MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
          MAL LT VIALTCLGG ASP PV PS  L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 1  MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60  GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
          GMYCAALESLINVS CSAI++TQRM  C  K +AGQ SS  RDTKIEV Q VK+LL
Sbjct: 61  GMYCAALESLINVSGCSAIEKTQRM LGGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130
          +++ ++R G F
Sbjct: 121 HLKKLFREGRF 131

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>gi|4504645|ref|NP_002179.1| (NM_002188) interleukin 13 [Homo sapiens]
gi|15297318|ref|XP_054534.1| (XM_054534) interleukin 13 [Homo sapiens]
gi|15297320|ref|XP_054533.1| (XM_054533) hypothetical protein XP_054533 [Homo sapie
gi|16171723|ref|XP_055221.1| (XM_055221) hypothetical protein XP_055221 [Homo sapie
* gi|462408|sp|P35225|IL13_HUMAN INTERLEUKIN-13 PRECURSOR (IL-13)
  gi|186276|gb|AAA36107.1| (L06801) interleukin 13 [Homo sapiens]
  gi|673420|emb|CAA48824.1| (X69079) alternative; ATG at 15 is an alternative start c
    sapiens]
  gi|1045452|gb|AAB01681.1| (U31120) interleukin-13 precursor [Homo sapiens]
  gi|14091716|gb|AAK53823.1|AF377331_1 (AF377331) interleukin 13 [Homo sapiens]
    Length = 132

```

Score = 169 bits (427), Expect = 5e-42

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

```

Query: 1  MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
          MAL LT VIALTCLGG ASP PV PS  L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 1  MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60  GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
          GMYCAALESLINVS CSAI++TQRM  C  K +AGQ SS  RDTKIEV Q VK+LL
Sbjct: 61  GMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130
          +++ ++R G F
Sbjct: 121 HLKKLFREGRF 131

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>gi|2144691|pir||A47481 interleukin-13 precursor - human
gi|580330|emb|CAA48823.1| (X69079) alternative; ATG at 15 is an alternative start c
    sapiens]
gi|445575|prf||1909326A interleukin 13 [Homo sapiens]
    Length = 146

```

Score = 167 bits (424), Expect = 1e-41

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

```

Query: 1  MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
          MAL LT VIALTCLGG ASP PV PS  L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 15 MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 74

```

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119  
 GMYCAALESLINVS CSAI++TQRM L C K +AGQ SS RDTKIEV Q VK+LL  
 Sbjct: 75 GMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 134

Query: 120 YVRGVYRHGNF 130  
 +++ ++R G F  
 Sbjct: 135 HLKCLFREGRF 145

>gi|7387804|sp|Q9XSV9|IL13\_BOVIN INTERLEUKIN-13 PRECURSOR (IL-13)  
 gi|5420145|emb|CAB46636.1| (AJ132441) interleukin-13 [Bos taurus]  
 Length = 132

Score = 161 bits (408), Expect = 8e-40  
 Identities = 87/131 (66%), Positives = 103/131 (78%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSP TLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59  
 MAL LT VI L C GGL SPSPV + LKELIEELVNITQNQ LCNGSMVWS+NLT+  
 Sbjct: 1 MALLLTAVIVLICFGGLTSPSPVPSATALKELIEELVNITQNQKVPLCNGSMVWSLNLTS 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119  
 MYCAAL+SLI++S+CS IQRT++ML ALC KP+A Q+SSE RDTKIEV Q +K+LL  
 Sbjct: 61 SMYCAALDSLISISNCSVIQRTTKMLNALCPHKPSAKQVSSEYVRDTKIEVAQFLKDLLR 120

Query: 120 YVRGVYRHGNF 130  
 + R V+R+ F  
 Sbjct: 121 HSRIVFRNERF 131

>gi|1127548|gb|AAA83738.1| (U10307) interleukin 13 [Homo sapiens]  
 Length = 131

Score = 160 bits (406), Expect = 1e-39  
 Identities = 92/131 (70%), Positives = 103/131 (78%), Gaps = 2/131 (1%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSP TLKELIEELVNITQNQAS-LCNGSMVWSVNLTA 59  
 MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ LCNGSMVWS+NLT+  
 Sbjct: 1 MALLLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKRPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119  
 GMYCAALESLINVS CSAI++TQRM L C K +AG SS RDTKIEV Q VK+LL  
 Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAG-FSSLHVRDTKIEVAQFVKDLLL 119

Query: 120 YVRGVYRHGNF 130  
 +++ ++R G F  
 Sbjct: 120 HLKCLFREGRF 130

>gi|4558814|gb|AAD22748.1|AF072807\_1 (AF072807) interleukin-13 precursor [Bos taurus]  
 Length = 114

Score = 146 bits (368), Expect = 3e-35  
 Identities = 81/113 (71%), Positives = 91/113 (79%), Gaps = 1/113 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSP TLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59  
 MAL LT VI L C GGL SPSPV + LKELIEELVNITQNQ LCNGSMVWS+NLT+

Sbjct: 1 MALLLTAVIVLICFGGLTSPSPVPSATALKELIEELVNITQNQKVPLCNGSMVWSLNLTS 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMALKALCSQKPAAGQISSERSRDTKIEVIQ 112  
MYCAAL+SLI++S+CS IQRT+RML ALC KP+A Q+SSE RDTKIEV Q

Sbjct: 61 SMYCAALDSLISISNCSVIQRTKRMLNALCPHKPSAKQVSSEYVRDTKIEVAQ 113

>gi|6680403|ref|NP\_032381.1| (NM\_008355) interleukin 13 [Mus musculus]  
gi|129377|sp|P20109|IL13\_MOUSE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION  
gi|91336|pir||E30552 T-cell activation protein P600 precursor - mouse  
gi|533247|gb|AAA40149.1| (M23504) T cell secreted protein [Mus musculus]  
Length = 131

Score = 143 bits (360), Expect = 3e-34

Identities = 79/134 (58%), Positives = 98/134 (72%), Gaps = 7/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSP----TLKELIEELVNITQNQASLCNGSMVWSVN 56  
MALW+T V+AL CLGGLA+P PV S TLKELIEEL NITQ+Q LCNGSMVWSV+

Sbjct: 1 MALWVTAVLALACLGGLAAPGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVD 60

Query: 57 LTAGMYCAALESLINVSDCSAIQRTQRMALKALCSQKPAAGQISSERSRDTKIEVIQLVKN 116  
L AG +C AL+SL N+S+C+AI RTQR+L LC++K A +SS DTKIEV +

Sbjct: 61 LAAGGFCVALDSLTNISNCNAIYRTQRILHGLCNRK-APTTVSS--LPDTKIEVAHFITK 117

Query: 117 LLTYVRGVYRHGNF 130

LL+Y + ++RHG F

Sbjct: 118 LLSYTKQLFRHGPF 131

>gi|14719448|pdb|1GA3|A Chain A, Nmr Structure Of Interleukin-13  
Length = 113

Score = 141 bits (355), Expect = 1e-33

Identities = 77/110 (70%), Positives = 88/110 (80%), Gaps = 1/110 (0%)

Query: 22 PVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80  
PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTAGMYCAALESLINVS CSAI++

Sbjct: 3 PVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 62

Query: 81 TQRMALKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130

TQRM L C K +AGQ SS RDTKIEV Q VK+LL +++ ++R G F

Sbjct: 63 TQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFRGRF 112

>gi|16758680|ref|NP\_446280.1| (NM\_053828) interleukin 13 [Rattus norvegicus]  
gi|1170528|sp|P42203|IL13\_RAT INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION P  
gi|2118664|pir||I52290 interleukin-13 - rat  
gi|438876|gb|AAA16478.1| (L26913) interleukin-13 [Rattus norvegicus]  
Length = 131

Score = 139 bits (350), Expect = 4e-33

Identities = 79/134 (58%), Positives = 99/134 (72%), Gaps = 8/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSV----TPSPTLKELIEELVNITQNQ-ASLCNGSMVWSV 55  
MALW+T V+AL CLGGLA+P PV +P L+ELIEEL NITQ+Q SLCN SMVWSV

Sbjct: 1 MALWVTAVLALACLGGLATPGPVRRSTSPVALRELIEELSNITQDQKTS LCNSSMVWSV 60



Query: 56 NLTAGMYCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVK 115  
 +LTAG +CAALES L N+S C+AI RTQR+L LC+QK A ++S DTKIEV Q +  
 Sbjct: 61 DLTAGGFCAALES LTNISSCNAIHRTQRI LNLGNLCNQK--ASDVASS-PPDTKIEVAQFIS 117

Query: 116 NLLTYVRGVYRHGN 129  
 LL Y + ++R+G+  
 Sbjct: 118 KLLNYSKQLFRYGH 131

>gi|258577|gb|AAB23881.1| P600 homolog [human, Peptide, 49 aa]  
 Length = 49

Score = 61.2 bits (147), Expect = 1e-09  
 Identities = 35/49 (71%), Positives = 36/49 (73%), Gaps = 1/49 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSPTLKE LIEELVNITQNQ-ASLCN 48  
 MAL LT VIAL CLGG SP PV PS L+ELIEEL NITQ Q A LCN  
 Sbjct: 1 MALLTTVIALACLGGFDSPGPVPPSTALRELIEELS NITQTQKAPLCN 49

>gi|451840|gb|AAA61629.1| (U05203) putative preprosperminogen [Oryctolagus cuniculus]  
 Length = 275

Score = 31.2 bits (69), Expect = 1.8  
 Identities = 21/71 (29%), Positives = 33/71 (45%), Gaps = 6/71 (8%)

Query: 16 GLASPSPTLKE LIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALES LINVSDC 75  
 G + PSPTL E +L+N+ LCN + ++ +TA CA S + C  
 Sbjct: 181 GYVKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRITASNL CAGYPSG-KIDTC 234

Query: 76 SAIQRTQRM LK 86  
 +Q+ +LK  
 Sbjct: 235 QRLQQLVEVLK 245

>gi|16760873|ref|NP\_456490.1| (NC\_003198) flagellar transcriptional activator [Salmo  
 enterica subsp. enterica serovar Typhi]  
gi|16503170|emb|CAD05675.1| (AL627272) flagellar transcriptional activator [Salmone  
 subsp. enterica serovar Typhi]  
 Length = 194

Score = 31.2 bits (69), Expect = 1.8  
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Query: 51 MVWSVNLTAGMYCAALES LINVSDCS---AIQRTQRM LKALCSQKPAAGQISSERS 103  
 M W N+ A M+C A + L+ CS A+ + R+ C Q P ++ R+  
 Sbjct: 67 MTWEQNIHASMFCNAWQFLK TGLCSGVDAVIKAYRLYLEQCPQPPEGSL LALTRA 122

>gi|7387658|sp|O52222|FLHC\_SALTY FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC  
gi|2772918|gb|AAB96640.1| (AF029300) FlhC [Salmonella typhimurium]  
gi|6045176|dbj|BAA85315.1| (D43640) FlhC protein [Salmonella typhimurium]  
 Length = 192

Score = 30.4 bits (67), Expect = 2.8  
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Sbjct: 44 ALECLGGVSGGGITDYNPALRSRLTIMKDDSKNQVSLSLSSV--TLEDATYYCA 96

>gi|15641617|ref|NP\_231249.1| (NC\_002505) conserved hypothetical protein [Vibrio cho  
gi|11354623|pir||C82178 conserved hypothetical protein VC1609 [imported] - Vibrio  
cholerae (group O1 strain N16961)  
gi|9656121|gb|AAF94763.1| (AE004238) conserved hypothetical protein [Vibrio cholera  
Length = 408

Score = 28.9 bits (63), Expect = 8.0

Identities = 18/48 (37%), Positives = 27/48 (55%), Gaps = 4/48 (8%)

Query: 2 ALWLTVVIALTCLGGLASPSVTPSPTLKELEE---LVNITQNQAS 45  
AL+ V+ LT GG+ S + P P K++ E +VN+ Q+QAS  
Sbjct: 39 ALFTNPVVVLTVFGGVVFYSFLYPLPYAKQIPREQTVSVVNLDQSQAS 86

Database: nr

Posted date: Nov 16, 2001 11:40 PM

Number of letters in database: 254,026,857

Number of sequences in database: 799,241

Lambda	K	H
0.319	0.131	0.381

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 60,265,884

Number of Sequences: 799241

Number of extensions: 1930804

Number of successful extensions: 5801

Number of sequences better than 10.0: 32

Number of HSP's better than 10.0 without gapping: 17

Number of HSP's successfully gapped in prelim test: 15

Number of HSP's that attempted gapping in prelim test: 5767

Number of HSP's gapped (non-prelim): 32

length of query: 131

length of database: 254,026,857

effective HSP length: 107

effective length of query: 24

effective length of database: 168,508,070

effective search space: 4044193680

effective search space used: 4044193680

T: 11

A: 40

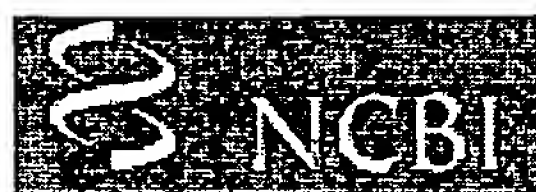
X1: 16 ( 7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.8 bits)

S2: 63 (28.9 bits)



Protein

PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Bio

Search  for 

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

GenPept

Save

Text

Add to Clipboard

☐ 1: P35225. INTERLEUKIN-13 PR...  
[gi:462408]

BLink, Related Sequences, OMIM, PubMed, Taxonomy,  
LinkOut

LOCUS IL13\_HUMAN 132 aa PRI 20-AUG-2001

DEFINITION INTERLEUKIN-13 PRECURSOR (IL-13).

\* ACCESSION P35225

PID g462408

VERSION P35225 GI:462408

DBSOURCE swissprot: locus IL13\_HUMAN, accession P35225;  
class: standard.  
extra accessions:043644,created: Feb 1, 1994.  
sequence updated: Feb 1, 1994.  
annotation updated: Aug 20, 2001.  
xrefs: gi: gi: 186275, gi: gi: 186276, gi: gi: 297787, gi: gi:  
673420, gi: gi: 580330, gi: gi: 1045451, gi: gi: 1045452, gi: gi:  
505626, gi: gi: 1127548, gi: gi: 2905619, gi: gi: 2905620, gi: gi:  
2144691, gi: gi: 1421355, gi: gi: 1421358  
xrefs (non-sequence databases): MIM 147683, InterPro IPR003634,  
InterPro IPR001325, ProDom PD015987, PROSITE PS00838

KEYWORDS Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 132)

AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,  
Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C.,  
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and  
Caput,D.

TITLE Interleukin-13 is a new human lymphokine regulating inflammatory  
and immune responses

JOURNAL Nature 362 (6417), 248-250 (1993)

MEDLINE 93211479

REMARK SEQUENCE FROM N.A.

REFERENCE 2 (residues 1 to 132)

AUTHORS McKenzie,A.N., Culpepper,J.A., Waal Malefyt,R., Briere,F.,  
Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de  
Vries,J.E., Banchereau,J. and Zurawski,G.R.

TITLE Interleukin 13, a T-cell-derived cytokine that regulates human  
monocyte and B-cell function

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3735-3739 (1993)

MEDLINE 93234572

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 132)

AUTHORS Dolganov,G., Lewis,D.B., Lovett,M., Burr,J., Bort,S., Short,D.,  
McGurn,M. and Gibson,C.

TITLE Direct Submission

JOURNAL Submitted (??-JUL-1995)

REMARK SEQUENCE FROM N.A.



Region 45  
/region\_name="Conflict"  
/note="A -> R (IN REF. 4)."  
Bond  
bond(48,76)  
/bond\_type="disulfide"  
Site 49  
/site\_type="glycosylation"  
/note="N-LINKED (GLCNAC...) (POTENTIAL)."  
Site 57  
/site\_type="glycosylation"  
/note="N-LINKED (GLCNAC...) (POTENTIAL)."  
Bond  
bond(64,90)  
/bond\_type="disulfide"  
Site 72  
/site\_type="glycosylation"  
/note="N-LINKED (GLCNAC...) (POTENTIAL)."  
Region 87  
/region\_name="Conflict"  
/note="S -> G (IN REF. 5)."  
Region 98  
/region\_name="Conflict"  
/note="MISSING (IN REF. 4)."  
Region 130  
/region\_name="Variant"  
/note="R -> Q. /FTId=VAR\_010037."

## ORIGIN

1 malllttvvia ltclggfasp gpvpstair elieelvnit qnqkaplcng smvwsinlta  
61 gmycaalesl invsgcsaie ktqrmlsgfc phkvsaggfs slhvrdrtkie vaqfvkdlll  
121 hlkklfregr fn

//

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